

GenCore version 5.1.3

Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: January 16, 2003, 16:40:32 : Search time 18 21.3 seconds
 (without alignments)
 56.562 Million cell updates/sec

Title: us-09-856-070-25

Perfect score: 23

Sequence: 1 MLRLQ 5

Scoring table:

BLOSUM62

Gap: 10.0, Gapext: 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	23	100.0	25	6 Q9BJ5	Q9BJ5 macaca fasc
2	23	100.0	25	6 Q9BJ4	Q9BJ4 pygathrix n
3	23	100.0	170	17 Q9GNA	Q9GNA aeropyrum p
4	23	100.0	143	10 Q9LW4	Q9LW4 oryza sativ
5	23	100.0	151	4 Q5P0C	Q5P0C homo sapien
6	23	100.0	156	4 Q9U28	Q9U28 homo sapien
7	23	100.0	157	17 Q9E576	Q9E576 archaetoglob
8	23	100.0	158	4 Q9U27	Q9U27 homo sapien
9	23	100.0	159	4 Q9U26	Q9U26 homo sapien
10	23	100.0	161	4 Q9U20	Q9U20 homo sapien
11	23	100.0	168	10 Q9LR06	Q9LR06 arabidopsis
12	23	100.0	173	10 Q9FJ3	Q9FJ3 arabidopsis
13	23	100.0	195	4 Q8W17	Q8W17 homo sapien
14	23	100.0	196	10 Q949T5	Q949T5 arabidopsis
15	23	100.0	196	13 Q9U08	Q9U08 ictalurus p
16	23	100.0	220	16 Q9E570	Q9E570 listeria in

17	23	100.0	220	16 Q9E578	Q9E578 listeria mo
18	23	100.0	256	4 Q9H611	Q9H611 homo sapien
19	23	100.0	272	16 Q9D57	Q9D57 listeria in
20	23	100.0	272	16 Q9E80	Q9E80 listeria mo
21	23	100.0	313	16 Q9Z015	Q9Z015 rhizobium m
22	23	100.0	322	16 Q9R08	Q9R08 xylella las
23	23	100.0	322	16 Q9Y62	Q9Y62 brucella me
24	23	100.0	323	2 Q8E118	Q8E118 rhodobacter
25	23	100.0	324	2 Q9E576	Q9E576 rhodobacter
26	23	100.0	323	16 Q8Y112	Q8Y112 talstonia s
27	23	100.0	326	5 Q94622	Q94622 trypanosoma
28	23	100.0	326	16 Q9M86	Q9M86 rhizobium l
29	23	100.0	328	16 Q9G27	Q9G27 bacillus ha
30	23	100.0	332	16 Q9A584	Q9A584 caulobacter
31	23	100.0	334	2 Q9F416	Q9F416 pseudomonas
32	23	100.0	348	5 Q9VW67	Q9VW67 drosophila
33	23	100.0	355	16 Q9E574	Q9E574 rhizobium m
34	23	100.0	364	16 Q9E579	Q9E579 agrobacteri
35	23	100.0	390	16 Q9XB25	Q9XB25 escherichia
36	23	100.0	427	4 Q9NX78	Q9NX78 homo sapien
37	23	100.0	440	17 Q9B364	Q9B364 methanococ
38	23	100.0	455	11 Q9VHK3	Q9VHK3 rattus norv
39	23	100.0	457	3 Q9P7X1	Q9P7X1 schizosacch
40	23	100.0	472	33 Q9N102	Q9N102 eptaleetus
41	23	100.0	478	5 Q9NDK8	Q9NDK8 leishmania
42	23	100.0	505	16 Q9D21	Q9D21 yersinia pe
43	23	100.0	517	16 Q9D12	Q9D12 rhizobium l
44	23	100.0	554	16 Q97TS2	Q97TS2 clostridium
45	23	100.0	560	5 Q9NKM3	Q9NKM3 leishmania

ALIGNMENTS

RESULT 1

Q9BGJ5	Q9BGJ5	PRELIMINARY;	PRT;	25 AA.
AC	Q9BGJ5			
DT	01-JUN-2001	(TRIMBLrel. 17, Created)		
DT	01-JUN-2001	(TRIMBLrel. 17, last sequence update)		
DT	01-DEC-2001	(TRIMBLrel. 19, last annotation update)		
DE	ATP synthase beta subunit (Fragment).			
OS	Macaca fascicularis (Crab-eating macaque) (Cynomolous monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopitheciinae; Macaca.			
OX	NCBI_TaxID=9541;			
EN	[1]			
FP	SEQUENCE FROM N A			
FX	MEDLINE=J1100552; PubMed=11156956;			
HA	Schmitz J., Ghazal M., Zischler H.;			
RI	"SINE insertions in Cladistic Analyses and the Phylogenetic			
RI	Affiliations of Tarsius bancanus to Other Primates.";			
RL	Genetics 157:777-784(2001).			
DR	EMBL; AF278735; AAK13310.1;			
FT	NON_TER	1		
FT	NON_TER	25		
SQ	SEQUENCE	25 AA;	2957 Mw;	4FHRL14C73A6A4w ChC64;
Query Match: 100.0%; Score 23; DB 6; Length 25;				
Best local similarity: 100.0%; Pred. No. 25;				
Matches: 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Q7	1 MLRLQ 5			
DB	18 MLRLQ 22			
RESULT 2				
Q9BGJ4	Q9BGJ4	PRELIMINARY;	PRT;	25 AA.
ID	Q9BGJ4			
AC	Q9BGJ4			
DT	01-JUN-2001	(TRIMBLrel. 17, Created)		

```

DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ATP synthase beta subunit (Fragment).
OS Pyruvate dehydrogenase (E1) subunit.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 21160452; PubMed 11156996;
RA Schmitz J., Ohme H., Zischner H.,
* "SINE insertions in Cladistia, Artibeus and the Phylogenetic
* Affiliations of Artibeus batobius to other Primates."
RL Genomics 157:777-784(2001).
DR EMBL: AF278736; AAK1311.1;
KW Nucleotide.
FT Nucleotide
SQ SEQUENCE 25 AA; 2957 MW; 41E8D144C71A6A4B CRC64;
Query Match 100.0%; Score 23; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRLQ 5
DB 18 MLRLQ 22
RESULT 3
QY99N8 PRELIMINARY: PRT: 120 AA.
AC QY99N8;
DI 01-NOV-1999 (TrEMBLrel. 12, Created)
DI 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein: APE2250.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN K1;
RX MEDLINE:99410439; PubMed:10482966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Naikawa Y.,
RA Jin no K., Takahashi M., Sekino M., Baba S.-I., Anai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kibeta K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA RES. 6:83-103(1999).
DR EMBL: AF000064; AAK1262.1;
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 120 AA; 13378 MW; B0B6E2538D542F9B CRC64;
Query Match 100.0%; Score 23; DB 17; Length 120;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRLQ 5
DB 1 MLRLQ 5
RESULT 4
QY10W4 PRELIMINARY: PRT: 133 AA.
AC QY10W4;
DI 01-OCT-2000 (TrEMBLrel. 15, Created)

```

```

DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Hypothetical 14.4 kDa protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX Using Y.C., Chow T., Chen C., Wu H., Chu M., Chao Y., Liu S.;
RA "Glyza sativa PAC P0699E04 genomes sequence, complete sequence."
RL Submitted (JAN 2002) to the EMBL/GenBank/TrEMBL databases.
DR EMBL: AF001111; AAY0505.1;
KW Hypothetical protein.
SQ SEQUENCE 133 AA; 14391 MW; 63B878295E6E32F3 CRC64;
Query Match 100.0%; Score 23; DB 10; Length 133;
Best Local Similarity 100.0%; Pred. No. 110;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRLQ 5
DB 108 MLRLQ 112
RESULT 5
QY9P00 PRELIMINARY: PRT: 151 AA.
AC QY9P00;
DI 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HSPC249.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-UMBILICAL CORD BLOOD;
RX MEDLINE:20499367; PubMed:11042152;
RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
RA Shen Y., Fan Y., Li G., Cheng M., Xu X.F., Han Z.G., Zhang J.W.,
RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously uncloned genes expressed in CD34+ hematopoietic
RT stem/progenitor cells."
RL Genome RES. 10:1546-1550(2000).
DR EMBL: AF151083; AAF46169.1;
DR InterPro: IPR000517; Ribosomal_L30.
DR Pfam: PF00327; Ribosomal_L30; 1.
SQ SEQUENCE 151 AA; 17499 MW; 9DA068C92D100C64 CRC64;
Query Match 100.0%; Score 23; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 120;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRLQ 5
DB 1 MLRLQ 5
RESULT 6
QY0JZ8 PRELIMINARY: PRT: 156 AA.
AC QY0JZ8;
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria, Primates, Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RE TISSUE-BRAIN;
 KA Chen Z.C., Fadiel A., Naftolin F.;
 RT "Mutation of erin gene in cancer."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DI EMBL: AF188896; AAF03154.1; -
 DP InterPro: IPR000299; Band_4.1
 DR InterPro: IPR000798; EzRad/moesin
 DR Pfam: PF00769; ERM; 1.
 DR PROSITE: PSS0057; BAND_41_3; 1.
 FT NON_TER 1 156
 FT NON_TER 156 156
 SQ SEQUENCE 156 AA; 19642 MW; 150PAA684A703A6 CRC64.

Query Match: 100.0%; Score 23; DB 4; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRQ 5
 DB 152 MLRQ 156

RESULT 7
 ID 028576 PRELIMINARY: PRT: 157 AA.
 AC 028576;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
 DE Hypothetical protein AF1697.
 GN AF1697.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RC SEQUENCE FROM N.A.
 RE STRAIN-VC-16 / DSM 4304 / ATCC 49658;
 RL MEDLINE=98049343; PubMed=9389475;
 RA Kirk H.-P., Clayton K.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Swinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.P., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty R.A., McKenney K., Adams M.D., Loftus R.,
 RA Peterson S., Reich C.L., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeck R., Gonyne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Springs T., Arlouch P., Kaine B.P., Sykes S.M.,
 RA Sadw P.W., Anders K.P., Rowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997)

CC - SIMILARITY: BELONGS TO THE ARSP FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS
 DR EMBL: AF00486; AAF0457.1
 DR TIGR: AF1697;
 DR InterPro: IPR001845; HTH_ARSR.
 DR Pfam: PF01022; HTH_5; 1.
 DR SMART: SM00418; HTH_ARSR; 1.
 KW DNA binding, Hypothetical protein, Transcription regulation,
 KW Complete proteome.
 SQ SEQUENCE 157 AA; 17478 MW; A00A270C7A7A5F9 CRC64;

Query Match: 100.0%; Score 23; DB 17; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRQ 5
 DB 152 MLRQ 156

DB 94 MLRQ 98
 RESULT 8
 ID 090JZ7 PRELIMINARY: PRT: 158 AA.
 AC 090JZ7;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAY-2002 (TEMBLrel. 20, Last annotation update)
 DE Erin (Fragment).
 DE Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RE TISSUE-Ovary;
 KA Chen Z.C., Fadiel A., Naftolin F.;
 RT "Erin gene mutation in ovarian cancer."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DI EMBL: AF188897; AAF03155.1; -
 DP InterPro: IPR000299; Band_4.1
 DR InterPro: IPR000798; EzRad/moesin.
 DR Pfam: PF00769; ERM; 1.
 DR PROSITE: PSS0057; BAND_41_3; 1.
 FT NON_TER 1 158
 FT NON_TER 158 158
 SQ SEQUENCE 158 AA; 19086 MW; 86192F70C6F2J57E CRC64;

Query Match: 100.0%; Score 23; DB 4; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRQ 5
 DB 151 MLRQ 155

RESULT 9
 ID 090JZ6 PRELIMINARY: PRT: 159 AA.
 AC 090JZ6;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAY-2002 (TEMBLrel. 20, Last annotation update)
 DE Erin (Fragment).
 DE Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 KA Fadiel A., Chen Z.C., Naftolin F.;
 RT "Mutation of erin gene in cancer."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DI EMBL: AF188898; AAF03156.1; -
 DP InterPro: IPR000299; Band_4.1
 DR InterPro: IPR000798; EzRad/moesin.
 DR Pfam: PF00769; ERM; 1.
 DR PROSITE: PSS0057; BAND_41_3; 1.
 FT NON_TER 1 159
 FT NON_TER 159 159
 SQ SEQUENCE 159 AA; 19244 MW; 7239898B7BA7A7A CRC64;

Query Match: 100.0%; Score 23; DB 4; Length 159;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRQ 5
 DB 151 MLRQ 155

DR InterPro: IPR004029; SL.
DR SMART: SM00316; S1; 1.
SQ SEQUENCE 168 AA; 19121 MW; 8F995484F5908C5 CRC64;

Query Match 100.0%; Score 23; DB 10; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.4e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRQ 5
DB 118 MLRQ 122
|||||

RESULT 12
Q9FJP3 PRELIMINARY; PRT; 173 AA.
AC Q9FJP3;
DT 01-MAR-2001 (TRENBLREL, 16, Created)
DI 01-MAR-2001 (TRENBLREL, 16, Last sequence update)
DT 01-JUN-2002 (TRENBLREL, 21, Last annotation update)
DE 50S ribosomal protein L29 (Putative 50S ribosomal protein L29).
GN A5C65220.
OS Arabidopsis thaliana (Mouse ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID:3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
Jiang P.X., Lee J.M., Onodera C.S., Quach H.H., Tang C., Toriumi M.,
Yamamura Y., Yu G., Yu S., Bowser L., Carrinci P., Chen H., Cheuk R.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
Ecker J.R., Theologis A.;
RT "Full Length cDNA of gene MN23.16/AT5g5220 (GI:10178184).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etou P., Lee J.M.,
Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
Southwick A., Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AH013395; BAB1658.1;
DR EMBL: AY045966; AAK76640.1;
DR EMBL: AY079351; AAL85082.1;
DR InterPro: IPR001854; Ribosomal_L29.
IP Pfam: Pf00041; Ribosomal_L29; 1.
DR TIGRfam: TIGR00012; L29; 1.
KW Ribosomal protein.
SQ SEQUENCE 173 AA; 19377 MW; H21246FC9464C142 CRC64;

Query Match 100.0%; Score 23; DB 10; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.4e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRQ 5
DB 91 MLRQ 95
|||||

